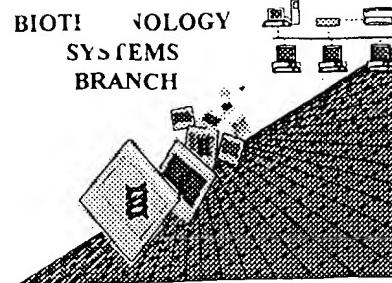


✓ Pak

#11

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/619,047 B

Source: 1652

Date Processed by STIC: 5-3-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Sequence Listing Error Summary

#11

## ERROR DETECTED    SUGGESTED    CORRECTION

SERIAL NUMBER: 09/619,047B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- |    |                                      |   |
|----|--------------------------------------|---|
| 1  | ____ Wrapped Nucleic                 | The number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".   |
| 2  | ____ Wrapped Aminos                  | The amino acid number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".  |
| 3  | ____ Incorrect Line Length           | The rules require that a line not exceed 72 characters in length. This includes spaces.   |
| 4  | ____ Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.   |
| 5  | ____ Non-ASCII                       | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.<br>Please ensure your subsequent submission is saved in ASCII text so that it can be processed.   |
| 6  | ____ Variable Length                 | Sequence(s) ____ contain n's or Xaa's which represented more than one residue.<br>As per the rules, each n or Xaa can only represent a single residue.<br>Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.   |
| 7  | ____ PatentIn ver. 2.0 "bug"         | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.                                |
| 8  | ____ Skipped Sequences (OLD RULES)   | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:<br><b>(2) INFORMATION FOR SEQ ID NO:X:</b><br><b>(i) SEQUENCE CHARACTERISTICS:</b> (Do not insert any headings under "SEQUENCE CHARACTERISTICS")<br><b>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:</b><br><b>This sequence is intentionally skipped</b><br><br>Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9  | ____ Skipped Sequences (NEW RULES)   | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.<br><b>&lt;210&gt; sequence id number</b><br><b>&lt;400&gt; sequence id number</b><br><b>000</b>  |
| 10 | ____ Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Use of <220> to <223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.  |
| 11 | ✓ Use of "Artificial" (NEW RULES)    | Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.<br><u>Valid response is Artificial Sequence.</u>   |
| 12 | ____ Use of <220>Feature (NEW RULES) | Sequence(s) ____ are missing the <220>Feature and associated headings.<br>Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"<br>Please explain source of genetic material in <220> to <223> section.<br>(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)  |
| 13 | ____ PatentIn ver. 2.0 "bug"         | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.  |

*V. Pak*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/619,047B

DATE: 05/03/2001  
TIME: 12:57:17

Input Set : A:\CHEM1110.ST25.txt  
Output Set: N:\CRF3\05032001\I619047B.raw

Does Not Comply  
Corrected Diskette Needed

See P.5

3 <110> APPLICANT: Chemicon International, Inc.  
 4 LENG, Jay  
 6 <120> TITLE OF INVENTION: PROTEASE SPECIFIC CLEAVABLE LUCIFERASES AND METHODS OF USE THEREOF  
 8 <130> FILE REFERENCE: CHEM1110  
 10 <140> CURRENT APPLICATION NUMBER: US 09/619,047B  
 11 <141> CURRENT FILING DATE: 2000-07-18  
 13 <160> NUMBER OF SEQ ID NOS: 29  
 15 <170> SOFTWARE: PatentIn version 3.0  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 936  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: *Renilla reniformis*  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: (1)..(936)  
 26 <400> SEQUENCE: 1

27 atg act tcg aaa gtt tat gat cca gaa caa agg aaa cg	48
28 Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr	
29 1 5 10 15	
31 ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca	96
32 Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser	
33 20 25 30	
35 ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att	144
36 Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile	
37 35 40 45	
39 ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg	192
40 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val	
41 50 55 60	
43 cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt	240
44 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly	
45 65 70 75 80	
47 atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat	288
48 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp	
49 85 90 95	
51 cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag	336
52 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys	
53 100 105 110	
55 aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat	384
56 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His	
57 115 120 125	
59 tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa	432
60 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu	
61 130 135 140	
63 agt gta gta gat gtt att gaa tca tgg gat gaa tgg cct gat att gaa	480,
64 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu	
65 145 150 155 160	
67 gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg gtt ttg	528

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/619,047B

DATE: 05/03/2001  
TIME: 12:57:17

Input Set : A:\CHEM1110.ST25.txt  
Output Set: N:\CRF3\05032001\I619047B.raw

68	Glu	Asp	Ile	Ala	Leu	Ile	Lys	Ser	Glu	Glu	Gly	Glu	Lys	Met	Val	Leu	
69				165					170							175	
71	gag	aat	aac	ttc	ttc	gtg	gaa	acc	atg	ttg	cca	tca	aaa	atc	atg	aga	
72	Glu	Asn	Asn	Phe	Phe	Val	Glu	Thr	Met	Leu	Pro	Ser	Lys	Ile	Met	Arg	
73				180					185						190		
75	aag	tta	gaa	cca	gaa	gaa	ttt	gca	gca	tat	ctt	gaa	cca	ttc	aaa	gag	
76	Lys	Leu	Glu	Pro	Glu	Glu	Phe	Ala	Ala	Tyr	Leu	Glu	Pro	Phe	Lys	Glu	
77		195					200				205						
79	aaa	ggg	gaa	gtt	cgt	cgt	cca	aca	tta	tca	tgg	cct	cgt	gaa	atc	ccg	
80	Lys	Gly	Glu	Val	Arg	Arg	Pro	Asp	Thr	Leu	Ser	Trp	Pro	Arg	Glu	Ile	Pro
81		210					215				220						
83	tta	gta	aaa	ggg	ggg	aaa	cct	gac	gtt	gta	caa	att	gtt	agg	aat	tat	
84	Leu	Val	Lys	Gly	Gly	Lys	Pro	Asp	Val	Val	Gln	Ile	Val	Arg	Asn	Tyr	
85		225					230			235				240			
87	aat	gct	tat	cta	cgt	gca	agt	gat	gat	tta	cca	aaa	atg	ttt	att	gaa	
88	Asn	Ala	Tyr	Leu	Arg	Ala	Ser	Asp	Asp	Leu	Pro	Lys	Met	Phe	Ile	Glu	
89		245					250			255							
91	tcg	gat	cca	gga	ttc	ttt	tcc	aat	gct	att	gtt	gaa	ggc	gcc	aag	aag	
92	Ser	Asp	Pro	Gly	Phe	Phe	Ser	Asn	Ala	Ile	Val	Glu	Gly	Ala	Lys	Lys	
93		260					265			270							
95	ttt	cct	aat	act	gaa	ttt	gtc	aaa	gta	aaa	ggg	ctt	cat	ttt	tcg	caa	
96	Phe	Pro	Asn	Thr	Glu	Phe	Val	Lys	Val	Lys	Gly	Leu	His	Phe	Ser	Gln	
97		275					280			285							
99	gaa	gat	gca	cct	gat	gaa	atg	gga	aaa	tat	atc	aaa	tcg	ttc	gtt	gag	
100	Glu	Asp	Ala	Pro	Asp	Glu	Met	Gly	Lys	Tyr	Ile	Lys	Ser	Phe	Val	Glu	
101		290					295			300							
103	cga	gtt	ctc	aaa	aat	gaa	caa	taa								936	
104	Arg	Val	Leu	Lys	Asn	Glu	Gln										
105	305					310											
108	<210>	SEQ	ID	NO:	2												
109	<211>	LENGTH:	311														
110	<212>	TYPE:	PRT														
111	<213>	ORGANISM:	Renilla reniformis														
113	<400>	SEQUENCE:	2														
115	Met	Thr	Ser	Lys	Val	Tyr	Asp	Pro	Glu	Gln	Arg	Lys	Arg	Met	Ile	Thr	
116	1				5				10						15		
119	Gly	Pro	Gln	Trp	Trp	Ala	Arg	Cys	Lys	Gln	Met	Asn	Val	Leu	Asp	Ser	
120					20				25					30			
123	Phe	Ile	Asn	Tyr	Tyr	Asp	Ser	Glu	Lys	His	Ala	Glu	Asn	Ala	Val	Ile	
124					35				40				45				
127	Phe	Leu	His	Gly	Asn	Ala	Ala	Ser	Ser	Tyr	Leu	Trp	Arg	His	Val	Val	
128					50				55			60					
131	Pro	His	Ile	Glu	Pro	Val	Ala	Arg	Cys	Ile	Ile	Pro	Asp	Leu	Ile	Gly	
132					65				70			75		80			
135	Met	Gly	Lys	Ser	Gly	Lys	Ser	Gly	Asn	Gly	Ser	Tyr	Arg	Leu	Leu	Asp	
136									85			90		95			
139	His	Tyr	Lys	Tyr	Leu	Thr	Ala	Trp	Phe	Glu	Leu	Leu	Asn	Leu	Pro	Lys	
140					100				105			110					
143	Lys	Ile	Ile	Phe	Val	Gly	His	Asp	Trp	Gly	Ala	Cys	Leu	Ala	Phe	His	

RAW SEQUENCE LISTING DATE: 05/03/2001  
 PATENT APPLICATION: US/09/619,047B TIME: 12:57:17

Input Set : A:\CHEM1110.ST25.txt  
 Output Set: N:\CRF3\05032001\I619047B.raw

144	115	120	125	
147	Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu			
148	130	135	140	
151	Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu			
152	145	150	155	160
155	Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu			
156	165	170	175	
159	Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg			
160	180	185	190	
163	Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu			
164	195	200	205	
167	Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro			
168	210	215	220	
171	Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr			
172	225	230	235	240
175	Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu			
176	245	250	255	
179	Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys			
180	260	265	270	
183	Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln			
184	275	280	285	
187	Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu			
188	290	295	300	
191	Arg Val Leu Lys Asn Glu Gln			
192	305	310		
195	<210> SEQ ID NO: 3			
196	<211> LENGTH: 936			
197	<212> TYPE: DNA			
198	<213> ORGANISM: Renilla reniformis (mutated sequence)			
200	<220> FEATURE:			
201	<221> NAME/KEY: CDS			
202	<222> LOCATION: (1)..(936)			
204	<400> SEQUENCE: 3			
205	atg act tcg aaa gtt tat gat cca gaa caa agg aaa cg <sup>48</sup> atg ata act			
206	Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr			
207	1 5 10 15			
209	gtt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca			96
210	Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser			
211	20 25 30			
213	ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att			144
214	Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile			
215	35 40 45			
217	ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg			192
218	Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val			
219	50 55 60			
221	cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt			240
222	Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly			
223	65 70 75 80			
225	atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat			288

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/619,047B

DATE: 05/03/2001  
TIME: 12:57:17

Input Set : A:\CHEM1110.ST25.txt  
Output Set: N:\CRF3\05032001\I619047B.raw

226 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp	
227               85               90               95	
229 cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag	336
230 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys	
231               100              105              110	
233 aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat	384
234 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His	
235               115              120              125	
237 tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa	432
238 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu	
239               130              135              140	
241 agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa	480
242 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu	
243 145              150              155              160	
245 gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg gtt ttg	528
246 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu	
247               165              170              175	
249 gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc atg aga	576
250 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg	
251               180              185              190	
253 aag tta gaa cca gac gaa gtt gac gca tat ctt gaa cca ttc aaa gag	624
254 Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu	
255               195              200              205	
257 aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa atc ccg	672
258 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro	
259               210              215              220	
261 tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg aat tat	720
262 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr	
263 225              230              235              240	
265 aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt att gaa	768
266 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu	
267               245              250              255	
269 tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc aag aag	816
270 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys	
271               260              265              270	
273 ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt tcg caa	864
274 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln	
275               275              280              285	
277 gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc gtt gag	912
278 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu	
279               290              295              300	
281 cga gtt ctc aaa aat gaa caa taa	936
282 Arg Val Leu Lys Asn Glu Gln	
283 305              310	
286 <210> SEQ ID NO: 4	
287 <211> LENGTH: 311	
288 <212> TYPE: PRT	
289 <213> ORGANISM: Renilla reniformis (mutated sequence)	
291 <400> SEQUENCE: 4	

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/619,047B

DATE: 05/03/2001  
TIME: 12:57:17

Input Set : A:\CHEM1110.ST25.txt  
Output Set: N:\CRF3\05032001\I619047B.raw

```

293 Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
294 1      5          10          15
297 Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
298      20         25          30
301 Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
302      35         40          45
305 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
306      50         55          60
309 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
310 65      70         75          80
313 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
314      85         90          95
317 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
318      100        105         110
321 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
322      115        120         125
325 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
326      130        135         140
329 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
330 145      150        155         160
333 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
334      165        170         175
337 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
338      180        185         190
341 Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu
342      195        200         205
345 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
346      210        215         220
349 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
350 225      230        235         240
353 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
354      245        250         255
357 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
358      260        265         270
361 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
362      275        280         285
365 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
366      290        295         300
369 Arg Val Leu Lys Asn Glu Gln
370 305      310

```

C--> 373 <210> SEQ ID NO: 5  
 374 <211> LENGTH: 8  
 375 <212> TYPE: PRT  
 376 <213> ORGANISM: Artificial  
 378 <220> FEATURE:  
 379 <223> OTHER INFORMATION: Description of Artificial Sequence: Protease recognition sequence  
 381 <400> SEQUENCE: 5  
 383 Ser Gln Asn Tyr Pro Ile Val Gln  
 384 1 5

Incomplete response as per section  
 1.8236 of new sequence rules. See  
 # 11 on the Error Summary Sheet.

The types of errors shown exist throughout the Sequence Listing. Please check  
 subsequent sequences for similar errors. Sequences 5-29.

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the  
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to  
 <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 05/03/2001  
PATENT APPLICATION: US/09/619,047B TIME: 12:57:18

Input Set : A:\CHEM1110.ST25.txt  
Output Set: N:\CRF3\05032001\I619047B.raw

L:376 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:389 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:402 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:415 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:428 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:441 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:454 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
L:467 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
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MAY 07 2001

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TECH CENTER 1600/2900

<110> Chemicon International, Inc.  
LENG, Jay

<120> PROTEASE SPECIFIC CLEAVABLE LUCIFERASES AND METHODS OF USE THEREOF

<130> CHEM1110

<140> US 09/619,047

<141> 2000-07-18

<160> 29

<170> PatentIn version 3.0

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48

ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca  
Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser  
20 25 30

96

ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att  
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile  
35 40 45

144

ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg  
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val  
50 55 60

192

cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt  
Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly  
65 70 75 80

240

atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat  
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp  
85 90 95

288

cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag  
His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys  
100 105 110

336

aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat  
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His  
115 120 125

384

tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa  
Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu  
130 135 140

432

agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa	480
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu	
145 150 155 160	
gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg gtt ttg	528
Glu Asp Ile Ala Leu Ile Lys Ser Glu Gly Glu Lys Met Val Leu	
165 170 175	
gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc atg aga	576
Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg	
180 185 190	
aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca ttc aaa gag	624
Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu	
195 200 205	
aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa atc ccg	672
Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro	
210 215 220	
tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg aat tat	720
Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr	
225 230 235 240	
aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt att gaa	768
Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu	
245 250 255	
tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc aag aag	816
Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys	
260 265 270	
ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt tcg caa	864
Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln	
275 280 285	
gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc gtt gag	912
Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu	
290 295 300	
cga gtt ctc aaa aat gaa caa taa	936
Arg Val Leu Lys Asn Glu Gln	
305 310	

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<212> PRT  
<213> Renilla reniformis

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1 5 10 15	

Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser	
20 25 30	

Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile  
 35 40 45

Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val  
 50 55 60

Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly  
 65 70 75 80

Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp  
 85 90 95

His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys  
 100 105 110

Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His  
 115 120 125

Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu  
 130 135 140

Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu  
 145 150 155 160

Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu  
 165 170 175

Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg  
 180 185 190

Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu  
 195 200 205

Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro  
 210 215 220

Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr  
 225 230 235 240

Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu  
 245 250 255

Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys  
 260 265 270

Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln

275

280

285

Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu  
 290 295 300

Arg Val Leu Lys Asn Glu Gln  
305 310

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1 5 10 15

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ggc ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca      96
Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
          20           25           30

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ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att 144  
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile  
35 40 45

ttt tta cat ggt aac gac gcc tct tct tat tta tgg cga cat gtt gtg 192  
 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val  
 50 55 60

cca cat att gag cca gta gcg cggttgt att ata cca gat ctt att ggt  
 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly  
 65 70 75 80

atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat 288  
 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp  
                   85              90              95

cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag	336	
His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys		
100	105	110

aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat	384
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His	
115                    120                    125	

tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa 432  
 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu  
 130 135 140

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agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa      480
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145          150          155          160

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gaa gat att gcg ttg atc aaa tct gaa gaa gaa aaa atg gtt ttg Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu	165                    170                    175	528
gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc atg aga Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg	180                    185                    190	576
aag tta gaa cca gac gaa gtt gac gca tat ctt gaa cca ttc aaa gag Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu	195                    200                    205	624
aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa atc ccg Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro	210                    215                    220	672
tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg aat tat Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr	225                    230                    235                    240	720
aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt att gaa Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu	245                    250                    255	768
tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc aag aag Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys	260                    265                    270	816
ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt tcg caa Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln	275                    280                    285	864
gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc gtt gag Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu	290                    295                    300	912
cga gtt ctc aaa aat gaa caa taa Arg Val Leu Lys Asn Glu Gln	305                    310	936
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Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser 20                    25                    30		
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile 35                    40                    45		
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val		

50

55

60

Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly  
 65                   70                   75                   80

Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp  
 85                   90                   95

His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys  
 100               105               110

Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His  
 115               120               125

Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu  
 130               135               140

Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu  
 145               150               155               160

Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu  
 165               170               175

Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg  
 180               185               190

Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu  
 195               200               205

Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro  
 210               215               220

Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr  
 225               230               235               240

Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu  
 245               250               255

Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys  
 260               265               270

Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln  
 275               280               285

Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu  
 290               295               300

Arg Val Leu Lys Asn Glu Gln  
305 310

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<223> Description of Artificial sequence: Protease recognition sequence

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1 5

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Pro Ser Pro Arg Glu Gly Lys Arg Ser Tyr  
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<400> 8

Tyr Val Ala Asp Gly  
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<210> 9  
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<213> Artificial sequence

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<223> Description of Artificial sequence: Protease recognition sequence

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Met Phe Gly Gly Ala Lys Lys Arg  
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<210> 10

<211> 10

<212> PRT

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<223> Description of Artificial sequence: Protease recognition sequence

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Gly Val Val Asn Ala Ser Ser Arg Leu Ala  
1 5 10

<210> 11

<211> 9

<212> PRT

<213> Artificial sequence

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<223> Description of Artificial sequence: Protease recognition sequence

<400> 11

Leu Ile Ala Tyr Leu Lys Lys Ala Thr  
1 5

<210> 12

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Val Lys Met Asp Ala Glu Phe  
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<210> 13

<211> 17

<212> PRT

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Phe Leu Ala Glu Gly Gly Val Arg Gly Pro Arg Val Val Glu Arg  
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His

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<220>  
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<400> 14

Asp Arg Val Tyr Ile His Pro Phe His Leu Val Ile His  
1 5 10

<210> 15  
<211> 8  
<212> PRT  
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<400> 15

Lys Pro Ala Leu Phe Phe Arg Leu  
1 5

<210> 16  
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<212> PRT  
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<220>  
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Ile Glu Pro Asp  
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<210> 19  
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<220>  
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<210> 20  
<211> 4  
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<220>  
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Asp Glu His Asp  
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<210> 21  
<211> 4  
<212> PRT  
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<220>  
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Asp Glu Val Asp  
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<210> 22  
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<400> 22

Xaa Glu His Asp  
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<210> 23  
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<220>  
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<220>  
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<222> (3)..(3)  
<223> Xaa is Ile or His

<400> 23

Val Glu Xaa Asp  
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<210> 24  
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<400> 24

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<220>  
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<400> 25

Leu Glu His Asp  
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<210> 26  
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<223> Xaa is any amino acid

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Xaa Xaa Xaa Asp

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<210> 27

<211> 8

<212> PRT

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<223> Description of Artificial sequence: Protease recognition sequence

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Arg Pro Leu Gly Ile Ile Gly Gly

1 5

<210> 28

<211> 3

<212> PRT

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<223> Description of Artificial sequence: Protease recognition sequence

<400> 28

Glu Gly Arg

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<210> 29

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Val Leu Lys

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